



FIG. 1

ATG GCT CGC CTA CAG ACT GCA CTC GTC GTT GTC CTC CTC GCT GTG GCG CTT CAA

GCA ACT GAG GCA GGC CCC TAC GGC GCC AAC ATG GAA GAC AGC GTC TGC TGC CGT GAT TAC

GTC CGT TAC CGT CTG CCC CTG CGC GTG GTG AAA CAC TTC TAC TGG ACC TCA GAC TCC TGC

CCG AGG CCT GGC GTG GTG TTG CTA ACC TTC AGG GAT AAG GAG ATC TGT GCC GAT CCC AGA

GTG CCC TGG GTG AAG ATG ATT CTC AAT AAG CTG AGC CAA TGA

AGAGCCTACTCTGATGACCGTGGCCCTTGGCTCCTCCAGGAAGGCTCAGGAGCCCTACCTCCCTGCCATTATAGCTGCTC

CCCGCCAGAGCCCTGTGCCAACTCTCTGCSATTCCCTGATCTCCATCCCTGTGGCTGTACCCCTTGGTCACCTCCGTGCT

GTCACTGCCATCTCCCCCTGACCCCTCTAACCCATCCTCTGCCTCCCTCCCTGCAGTCAGAGGTCCTGTTCCCATCA

GCGATTCCCCCTGCTTAACCCCTTCCATGACTCCCCCACTGCCCTAAGCTGAGTCACTCTCCCAAGCCTGGCATGTGGCC

CTCTGGATCTGGGTTCCATTCTGTCTCCAGCCTGCCCACTTCCCTTCATGAATGTTGGTTCTAGCTCCCTGTTCTCC

AAACCCATACTACATCCCACTTCTGGGTCTTTGCCTGGGATGTTGCTGACACTCAGAAAGTCCCGTCGACGCGGCC

FIG. 3A-1
FIG. 3A-2
FIG. 3A-3

FIG. 3A

GTGACCCACGGTCCGCGCCGAGAACCCGCAATCTTTGCGCCACAAATACCCGACGATGCCCGATCTACTTTAAG	79
GGCTGAACCCACGGCCCTGAGAGACTATAAGAGCGTTCCTACCGCC	7
ATG GAA CAA CCG GGA CAG AAC	148
A P A A S G A R K R H G P G P R E A R G	27
GCC CCG GCC GCT TCG CGG GCC CGG AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA	208
A R P G L R V P K T L V L V V A A V L L	47
GCC AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT GTC GCC GCG GTC CTC CTG	268

L	V	S	A	E	S	A	L	I	T	Q	Q	D	L	A	P	Q	Q	R	A	67
TTG	GTC	TCA	GCT	GAG	TCT	GCT	CTG	ATC	ACC	CAA	CAA	GAC	CTA	GCT	CCC	CAG	CAG	AGA	GCG	328
A	P	Q	Q	K	R	S	S	P	S	E	G	L	C	P	P	G	H	H	I	87
GCC	CCA	CAA	CAA	AAG	AGG	TCC	AGC	CCC	TCA	GAG	GGA	TTG	TGT	CCA	CCT	GGA	CAC	CAT	ATC	388
S	E	D	G	R	D	C	I	S	C	K	Y	G	Q	D	Y	S	T	H	W	107
TCA	GAA	GAC	GGT	AGA	GAT	TGC	ATC	TCC	TGC	AAA	TAT	GGA	CAG	GAC	TAT	AGC	ACT	CAC	TGG	448
N	D	L	L	F	C	L	R	C	T	R	C	D	S	G	E	V	E	L	S	127
AAT	GAC	CTC	CTT	TTC	TGC	TTG	CGC	TGC	ACC	AGG	TGT	GAT	TCA	GGT	GAA	GTG	GAG	CTA	AGT	508
F	C	T	T	T	R	N	T	V	C	Q	C	E	E	G	T	F	R	E	E	147
CCC	TGC	ACC	ACG	ACC	AGA	AAC	ACA	GTG	TGT	CAG	TCC	GAA	GAA	GGC	ACC	TTC	CGG	GAA	GAA	568
D	S	P	E	M	C	R	K	C	R	T	G	C	P	R	G	M	V	K	V	167
GAT	TCT	CCT	GAG	ATG	TGC	CGG	AAG	TGC	CGC	ACA	GGG	TGT	CCC	AGA	GGG	ATG	GTC	AAG	GTC	628
G	D	C	T	P	W	S	D	I	E	C	V	H	K	E	S	G	T	K	H	187
GGT	GAT	TGT	ACA	CCC	TGG	AGT	GAC	ATC	GAA	TGT	GTC	CAC	AAA	GAA	TCA	GGT	ACA	AAG	CAC	688
S	G	E	A	P	A	V	E	E	T	V	T	S	S	P	G	T	P	A	S	207
AGT	GGG	GAA	GCC	CCA	GCT	GTG	GAG	GAG	ACG	GTG	ACC	TCC	AGC	CCA	GGG	ACT	CCT	GCC	TCT	748

Applicant: Douglas A. Holtzman et al.
 Title: NOVEL GENES ENCODING PROTEINS HAVING
 PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC
 AND OTHER USES

Attorney/Agent: Jean M. Silveri
 Docket No.: MPI2000-540OMNI(M)

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P	C	S	L	S	G	I	I	I	G	V	T	V	A	A	V	V	L	I	V	227
CCC	TGT	TCT	CTC	TCA	GGC	ATC	ATC	ATA	GGA	GTC	ACA	GTT	GCA	GCC	GTA	GTC	TTG	ATT	GTG	808
A	V	F	V	C	K	S	L	L	W	K	K	V	L	P	Y	L	K	G	I	247
GCT	GTG	TTT	GTT	TGC	AAG	TCT	TTA	CTG	TGG	AAG	AAA	GTC	CTT	CCT	TAC	CTG	AAA	GGC	ATC	868
C	S	G	G	G	G	D	P	E	R	V	D	R	S	S	Q	R	P	G	A	267
TGC	TCA	GGT	GGT	GGT	GGG	GAC	CCT	GAG	CGT	GTG	GAC	AGA	AGC	TCA	CAA	CGA	CCT	GGG	GCT	928
E	D	N	V	L	N	E	I	V	S	I	L	Q	P	T	Q	V	P	E	Q	287
GAG	GAC	AAT	GTC	CTC	AAT	GAG	ATC	GTG	AGT	ATC	TTG	CAG	CCC	ACC	CAG	GTC	CCT	GAG	CAG	988
E	M	E	V	Q	E	P	A	E	P	T	G	V	N	M	L	S	P	G	E	307
GAA	ATG	GAA	GTC	CAG	GAG	CCA	GCA	GAG	CCA	ACA	GGT	GTC	AAC	ATG	TTG	TCC	CCC	GGG	GAG	1048
S	E	H	L	L	E	P	A	E	A	E	R	S	Q	R	R	R	L	L	V	327
TCA	GAG	CAT	CTG	CTG	GAA	CCG	GCA	GAA	GCT	GAA	AGG	TCT	CAG	AGG	AGG	AGG	CTG	CTG	GTT	1108
P	A	N	E	G	D	P	T	E	T	L	R	Q	C	F	D	D	F	A	D	347
CCA	GCA	AAT	GAA	GGT	GAT	CCC	ACT	GAG	ACT	CTG	AGA	CAG	TGC	TTC	GAT	GAC	TTT	CCA	GAC	1168
L	V	P	F	D	S	W	E	P	L	M	R	K	L	G	L	M	D	N	E	367
TTG	GTG	CCC	TTT	GAC	TCC	TGG	GAG	CCG	CTC	ATG	AGG	AAG	TTG	GGC	CTC	ATG	GAC	AAT	GAG	1228

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FIG. 3A-3

FIG. 3B-1
FIG. 3B-2
FIG. 3B-3

FIG. 3B

I	K	V	A	K	A	E	A	A	G	H	R	D	T	L	Y	T	M	L	I	387
ATA	AAG	GTG	GCT	AAA	GCT	GAG	GCA	GCG	GCC	CAC	AGG	GAC	ACC	TTG	TAC	ACG	ATG	CTG	ATA	1288
K	W	V	N	K	T	G	R	D	A	S	V	H	T	L	L	D	A	L	E	407
AAG	TGG	GTC	AAC	AAA	ACC	GGG	CGA	GAT	GCC	TCT	GTC	CAC	ACC	CTG	CTG	GAT	GCC	TTG	GAG	1348
T	L	G	E	R	L	A	K	Q	K	I	E	D	H	L	L	S	S	G	K	427
ACG	CTG	CGA	GAG	AGA	CTT	GCC	AAG	CAG	AAG	ATT	GAG	GAC	CAC	TTG	TTG	AGC	TCT	CGA	AAG	1408
F	M	Y	L	E	G	N	A	D	S	A	M	S	*							441
TTC	ATG	TAT	CTA	GAA	GGT	AAT	GCA	GAC	TCT	GCC	ATG	TCC	TAA							1450

FIG. 3B-1 6/31

GTGTGATTCCTTCAGGAAGTGAGACCTTCCCTCGTTTACCTTTTTCCTCGAATAAGCCCACTCGACTCCAGTCAGTA 1529
 GGAAAGTGCCACAAATTGTACATGACCGGTACTCGAAGAACTCTCCCATCCAACATCACCCAGTGGATCGAACAATCCT 1608
 GTAACCTTTCACCTGCACCTTGGCAATTAATTTTAAGCTGAATGTGATAATAAGGACACTATCGAAATGCTCTCGATCATT 1687
 CCGTTTGTGCGTACTTTCGAGATTTCGTTTGGGATGTCTATTTTCACAGCACCTTTTTCATCCTTAAATGCTTAA 1766
 TTTATTTTATTTGGGCTACATTGTGAAGATCCATCTACACAGTCGTTGTCCGACTTCACCTTGAATCTATATGATGAACC 1845
 TTTTTCGGTGGGGTGCNGGCCAATTCCACTCTGTCTCCAGGCTGGAGTGCAATGCTGCAATCTTGGCTCACTATA 1924
 GCCTTGACCTCTGAGGCTCAAGCGATTCTCTCACCTCAGCCATCCAAATAGCTGGGACCAACAGGTGTGCACCACCCACGC 2003
 CCGGCTAATTTTTCGTAATTAAGGGCTCTCTATGTGTCTCAGGGTGTCTCGAATTCCTCGGACTCAAG 2082
 CAGTCTGCCACATCAGACTCCCAAAGGGTGGAAATTAGARGCGTGAGCCCCCATGCTTGGCCCTTACCTTTCCTACTTTT 2161
 TATAATTCGTATGTTATTAATTTATGAACATCAAGAACTTTAGTAAATGTACTTGTTTTACATAGTTATGTGCAATAGA 2240
 TTAGATAAACATAAAGGAGGAGACATACAAATGGGGGAAGAAGAAGTCCCTGTGAAGAAGTTNACGNTCTGGTTTC 2319

CAGCCTTCCCTCAGATGTACTTTGGCTTCAATGATTGGCAACTTCTACAGGGGCCAGTCTTTTGAACCTGGACAACCTTA 2398

CAAGTATATGAGTATTATTATAGGTAGTTGTATTACATATGAGTCGGGACCAAGAGAACTGGATCCACGTCAAGTCCT 2477

GTTGTGGCTGGTCCCTACCTGGGCAGTCTCATTTTCACCCCATAGCCCCCATCTATGGACAGGCTGGGACAGAGGCAGA 2556

TGGGTTAGATCACACATAACAAATAGGGTCTATGTTCATATCCCAAGTGAACCTTGAGCCCTGTTTGGGCTCAGGAGATAGA 2635

AGACAAAATCTGTCTCCACGTCCTGCCATGGCATCAAGGGGAAGAGTAGATGGTGCTTGAGAAATGGGTT 2714

GCCATCTCAGGAGTAGATGCCCGGCTCATTCTGGTTATCTGTCAACCCTGAGCCCATGAGCTGCCCTTTTAGGGTACAG 2793

ATTGCCCTACTTGAGGACCTTGGCGCGCTCTGTAAAGCATCTGACTCATCTCAGAAATGTCAATTCTTAAACACTGTGGCAA 2872

CAGGACCTAGAAATGGCTGACGCATTAAAGGTTTTCMTCTGTCCTGTTCTATTATTTGTTTAAAGACCTCAGTAACCAT 2951

TTACGCCCTCTTTCCAGCAACCCCTTCTCCATAGTATTTCAGTCAATGGAAGGATCATTTATGCAAGGTAGTCAATCCAGGA 3030

GTTTTGTGCTTTCTGTCTCAAGGCAATGTGTGTTTGTGTTTCCGGACTGGTTGGGTGGGACAAAGTTAGAAATTGCCT 3109

GAAGATCACACATTCAGACTGTTGTGTCTGTGAGTTTATAGGAGTGGGGGTGACCTTCTGGTCTTTCACCTTCCATC 3188

CTCTCCACTTCCATCTGGCATCCACGGGTTGTCCCTGCATTTCTGGAAGGCACAGGGTGCTGCTGCCCTCCTGGTCT 3267

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FIG. 3B-3

TTGCCCTTGGCTCGGCCCTTCTGTCCAGGACGCTCAGCCTCAGGGCTCAGAAGGTGCCAGTCCCGTCCAGGTCCCTTGTC 3346
 CCTTCCACAGAGGCCTTCCCTAGAAGATGCACTCTAGAGTGTGAGCCCTTATCAGTGTTTAAGATTTTTCCTTTTATTTTAA 3425
 TTTTTTTIGAGACAGAACTCTCACTCTCTCTGCCAGGCTCGGAGTGCACCGGTACGATCTTTGGCTCAGTGCACCTCCGCCT 3504
 CCTGGGTTCAAGCGATTCTCGTGCCCTCAGCCTCCGGAGTAGCTGGGATTCAGGACCCGCCACCCAGCCCTGGTTAATT 3583
 TTGTATTTTTTAGTAGACGGGGTTTTCACCATGTTGGTCAGGCTGGTCTCGAATCTCTGACCTCAGGTGATCCACCTT 3662
 GGCCTCCGAAAGTCTCGGATTACAGGGGTGAGCCACCAGCCAGGCCAAGCTATTCTTTTAAAGTAAGCTTCCCTGACGA 3741
 CATGAAATAATTGGGGGTTTGTGTGTTTGTATTAATTAGGCTTTTGTCTATATATCCAGGCCAAATAGCATGTGACACAGG 3820
 ACAGCCATAGTATAGTGTCTACTCGTGGTGGTGTCTCTTTTCATGCTTCTGCCCCTGTCAAAAGGTCCCTATTGTAAATGT 3899
 GTTATAATACAAACAAGGAAGCACATTGTGTACAAAATACTTATGTATTTATCGAATCCATGACCACAAATTAAATATGAAA 3978
 CCTTATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGSGGGGGGGCCG 4051

FIG. 3C

FIG. 4A-1
FIG. 4A-2
FIG. 4A-3

FIG. 4A

GTGACCCACGGTCCGGCCGGAGAACCCGCAATCTTTGCGCCCAAAATACACCGACGATCCCCGATCTACTTTAAG	79
GGCTGAAACCCACGGGCTGAGAGACTATAAGAGCGTTCCCTACGGCC ATG GAA CAA CCG CGA CAG AAC	148
A P A A S G A R K R H G P G P R E A R G	27
GCC CCG GCC GCT TCG GGG GCC CCG AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA	208
A R P G L R V P K T L V L V A A V L L	47
GCC AGG CCT GGG CTC CCG GTC CCC AAG ACC CTT GTG CTC GTT GTC GCC GCG GTC CTC CTG	268

FIG. 4A-1

L V S A E S A L I T Q Q D L A P Q Q R A 67
 TTG GTC TCA GCT GAG TCT GCT ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 328

 A P Q Q K R S S P S E G L C P P G H H I 87
 GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG TGT CCA CCT GGA CAC CAT ATC 388

 S E D G R D C I S C K Y G Q D Y S T H W 107
 TCA GAA GAC GGT AGA GAT TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC TCG 448

 N D L L F C L R C T R C D S G E V E L S 127
 AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT GAT TCA CGT GAA GTG GAG CTA AGT 508

 P C T T R N T V C Q C E E G T F R E E 147
 CCC TGC ACC ACG ACC AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG GAA GAA 568

 D S P E M C R K C R T G C P R G M V K V 167
 GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA GGG TGT CCC AGA GGG ATG GTC AAG GTC 628

 G D C T P W S D I E C V H K E S G I I I 187
 GGT GAT TGT ACA CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC ATC ATC ATA 688

 G V T V A A V V L I V A V F V C K S L L 207
 GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG 748

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FIG. 4A-2

W	K	K	V	L	P	Y	L	K	G	I	C	S	G	G	G	D	P	E	227
TGG	AAG	AAA	GTC	CTT	CCT	TAC	CTG	AAA	GGC	ATC	TGC	TCA	GGT	GGT	GGT	GAC	CCT	GAG	808
R	V	D	R	S	S	Q	R	P	G	A	E	D	N	V	L	N	E	I	V
CGT	GTG	GAC	AGA	AGC	TCA	CAA	CGA	CCT	GGG	GCT	GAG	GAC	AAT	GTC	CTC	AAT	GAG	ATC	GTG
S	I	L	Q	P	T	Q	V	P	E	Q	E	M	E	V	Q	E	P	A	E
AGT	ATC	TTG	CAG	CCC	ACC	CAG	GTC	CCT	GAG	CAG	GAA	ATG	GAA	GTC	CAG	GAG	CCA	GCA	GAG
P	T	G	V	N	M	L	S	P	G	E	S	E	H	L	L	E	P	A	E
CCA	ACA	GGT	GTC	AAC	ATG	TTG	TCC	CCC	GGG	GAG	TCA	GAG	CAT	CTG	CTG	GAA	CCG	GCA	GAA
A	E	R	S	Q	R	R	R	L	L	V	P	A	N	E	G	D	P	T	E
GCT	GAA	AGG	TCT	CAG	AGG	AGG	CTG	CTG	GTT	CCA	GCA	AAT	GAA	GGT	GAT	CCC	ACT	GAG	1048
T	L	R	Q	C	F	D	D	F	A	D	L	V	P	F	D	S	W	E	P
ACT	CTG	AGA	CAG	TGC	TTC	GAT	GAC	TTT	GCA	GAC	TTG	GTG	CCC	TTT	GAC	TCC	TGG	GAG	CCG
L	M	R	K	L	G	L	M	D	N	E	I	K	V	A	K	A	E	A	A
CTC	ATG	AGG	AAG	TTG	GGC	CTC	ATG	GAC	AAT	GAG	ATA	AAG	GTG	GCT	AAA	GCT	GAG	GCA	GCG
G	H	R	D	T	L	Y	T	M	L	I	K	W	V	N	K	T	G	R	D
GGC	CAC	AGG	GAC	ACC	TTG	TAC	ACG	ATG	CTG	ATA	AAG	TGG	GTC	AAC	AAA	ACC	GGG	CGA	GAT

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FIG. 4A-3

20250304T0600

Applicant: Douglas A. Holtzman et al.
Title: NOVEL GENES ENCODING PROTEINS HAVING
PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC
AND OTHER USES

Attorney/Agent: Jean M. Silveri
Docket No.: MPI2000-540OMNI(M)
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FIG. 4B-1
FIG. 4B-2
FIG. 4B-3

FIG. 4B

A	S	V	H	T	L	L	D	A	L	E	T	L	G	E	R	L	A	K	Q		387
GCC	TCT	GTC	CAC	ACC	CTG	CTG	GAT	GCC	TTG	GAG	ACG	CTG	GGA	GAG	AGA	CTT	GCC	AAG	CAG		1288
K	I	E	D	H	L	L	S	S	G	K	F	M	Y	L	E	G	N	A	D		407
AAG	ATT	GAG	GAC	CAC	TTG	TTG	AGC	TCT	GGA	AAG	TTC	ATG	TAT	CTA	GAA	GGT	AAT	GCA	GAC		1348
S	A	M	S	*																412	
TCT	GCC	ATG	TCC	TAA																1363	

FIG. 4B-1

GTGTGATTCCTCTCAGGAAGTGAGACCTTCCCTCGTATTACCTTTTTCCTGGAAAAAGCCCAACTGGACTCCAGTCAGTA 1442
 CGAAAGTCCCAACAATTGTTCACATGACCGGTACTCGAAGAAACTCTCCCATCCAAACATCACCAGTGGATGGAACATCCT 1521
 GTAACATTTTCACCTGCACTTGGCAATTATTTTATTAAGCTGAATGTGATTAATAAGGACACATATGGAAAATGCTCTGGATCATTT 1600
 CCGTTTGTGGTACTTTTGAGATTGGTTTGGGATGTCATTTGTTCACAGCACATTTTMMTATCCTAATGTAAATGCTTTTA 1679
 TTTATTTTATTTGGGCTACATTGTGAAGATCCATCTACACAGTCTGTTCGACCTTCGACCTTCACCTTACTATATGATATGAAC 1758
 TTTTTCGGGTGGGGGTGTCNGGGCAATTCCACTCTGTCTCCAGCCTGGAGTGCATATGTTGCAATCTTCGGCTCCTACTATA 1837
 GCCTTGACCTCTGAGGCTCAAGCGATTCTCTCACCCTCAGCCATCCAAATAGCTGGGACCAACAGGTGTGCACCAACCAACGC 1916
 CCGGCTAAATTTTTCGTATTTTGTCTAAATATAAGGGCTCTCTATATTTGCTCAGGGTGGTCTCGGAATTCCTGGACTCAAG 1995
 CAGTCTGCCCCACYTCAGACTCCCAAGCGGTGGAAATTAGARGCGTGAGCCCCCATGCTTTGGCCTTACCTTTCTACTCTTTT 2074
 TATAATTCCTGTATGTTATTTTATGAACATGAAGAAACTTTTAGTAAATGTACTTTGTTTACATAGTTATGTGAATAGA 2153
 TTAGATAACATAAAGGAGAGACATACAATGGGGGAAGAAGAAGTCCCTTGTAAAGATTNACCTCTGGTTTC 2232
 CAGCCTTCCCTCAGATGTACTTTTGGCTTCAATGATTGGCAACTTCTACAGGGGCCAGTCTTTTGTGAACCTGGACAACCTTA 2311

CAAGTATATGAGTATTATTATAGGTAGTGTGTTACATATGAGTCGGGACCAAGAGAACTGGATCCACGTGAAGTCCT 2390

GTGTGTGGCTGGTCCCTACCTGGCCAGTCTCTCATTTGCACCCCATAGCCCCCATCTATGGACAGGCTGGGACAGAGGCAGA 2469

TGGGTTAGATCACACATAACAAATAGGGTCTATGTTCATATCCCAAGTGAACCTMGAGCCCTGTCTTGGGCTCAGGAGATAGA 2548

AGACAAAATCTGTCTCCACGCTCTGCCATGGCATCAAGGGGGAAGAGTAGATGGTCTTGAGAAATGGTGTGAAAATGGTT 2627

GCCATCTCAGGAGTAGATGGCCCGGCTCAGCTTCTGGTTATCTGTACCCCTGAGCCCATGAGCTCCCTTTTACGGGTACAG 2706

ATTGCCCTACTTGTAGGACCTTGGCCCGCTCTGTAAAGCATCTGACTCATCTCAGAAATGTCAATTTCTTAAACACTGTGCGAA 2785

CAGGACCTAGAAATGGCTGACGCATTAAAGGTTTCTTCTGTGTCTCTGTCTTCTATTTATTTTAAAGACCTCAGTAACCAT 2864

TTTACAGCCTCTTTTCCAGCAAACCCCTCTCCATAGTATTTTTCAGTCAATGGAAGGATCATTTTATGTCAGGTAGTCAATCCAGGA 2943

GTTTTGGTCTTTTCTGCTCTCAAGGCAATGTGTGTCTTGTGTCTCTGTCTCTTCTATTTATTTTGGGTGGGACAAAGTTAGAAATTCCT 3022

GAAGATCACACATTCAGACTGTGTGTCTGTGTGAGTTTATAGGAGTGGGGGTGACCTTTTCTGGTCTTTTGCACCTTCCATC 3101

CTCTCCCACTTCCATCTGGCATCCCAAGGCTGTGTCCTCTGCACCTTCTGGAAGGCACAGGGTGTCTGTCTCTCTGGTCT 3180

TTGCCCTTTGTCTGGGCTTCTGTGTCAGGACGCTCAGGCTCAGAGGCTCAGAGGTTGCCAGTCCGTCAGGTCCTTGTCT 3259

CCTTCCACAGAGCCCTTCCTAGAGAAGATGCACTCTAGAGTGTACGCCCTTATCAGTGTATTAGATTTCCTCTTTTAA 3338
 TTTTTCGAGACAGAAATCTCACTCTCTCGCCAGGCTGGAGTGCAAGGTACGATCTTTGGCTCAGTGCACCTCCGCCCT 3417
 CCTGGGTTCAGCGATTCCTCGTGCCTCAGCCTCCGGAGTAGCTGGGATTCCAGGCACCCGCCACCAAGCCCTGGTTAATT 3496
 TTTGTATTTTTFAGTAGAGACGGGGTTTCACCACTGTGTGCTCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCACCTT 3575
 GGCCTCCGAAAGTGTCTGGGATTACAGGGGTGAGCCACAGCCAGGCCCAAGCTATTCTTTTAAAGTAAGCTTTCCTGACGA 3654
 CATGAAATAATTGGGGGTTTGTGTGTTAGTTACATTAGGCTTTGCTATATCCCAAGGCCAAATAGCATGTGACACACAGG 3733
 ACAGCCATAGTATAGTGTCTCACTCGTGGTGGTGTCTCTTTCAATGCTTGTCCCTGTGCAAAAGGTCCCTATTTCGAAATGT 3812
 GTTATAATACAAACAAGGAAGCACATTGTGTACAAAATACTTATGTATTTATGAAATCCATGACCAAAATTAAATATGAAA 3891
 CCTTATATAAGGGGGGGGGGGGG 3964

FIG. 4C

FIG. 5A-1
FIG. 5A-2
FIG. 5A-3

FIG. 5A

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CCACGGCTCCGGCGGGCGCTCCGCTGAGGGACGGCGGGAGCGCGCGCTGGCCCTCGCACTCAAAGCCGCCAGCCG 79

GCCCCGGCTCGGCCGACCCGGCGGGGATCTAGGGGTGGCCGACTMYCCCGGACCGTGGCCGCACTGTMYCTGGGAGTTA 158

CTGATCATCTTCTTTGAAGAAAC ATG AAG TTA CAC TAT GTT GCT GTG CTT ACT CTA GCC ATC CTG 223

ATG TTC CTG ACA TGG CTT CCA GAA TCA CTG AGC TGT AAC AAA GCA CTC TGT GCT AGT GAT 283

FIG. 5A-1

V	S	K	C	L	I	Q	E	L	C	Q	C	R	P	G	E	G	N	C	S	54
GTG	AGC	AAA	TGC	CTC	ATT	CAG	GAG	CTC	TGC	CAG	TGC	CGG	CCG	GGA	GAA	GGC	AAT	TGC	TCC	343
C	C	K	E	C	M	L	C	L	G	A	L	W	D	E	C	C	D	C	V	74
TGC	TGT	AAG	GAG	TGC	ATG	CTG	CTG	TGT	GGG	GCC	CTT	TGG	GAC	GAG	TGC	TGT	GAC	TGT	GTT	403
G	M	C	N	P	R	N	Y	S	D	T	P	P	T	S	K	S	T	V	E	94
GGT	ATG	TGT	AAT	CCT	CGA	AAT	TAT	AGT	GAC	ACA	CCT	CCA	ACT	TCA	AAG	AGC	ACA	GTG	GAG	463
E	L	H	E	P	I	P	S	L	F	R	A	L	T	E	G	D	T	Q	L	114
GAG	CTG	CAT	GAA	CCG	ATC	CCT	TCT	CTC	TTC	CGG	GCA	CTC	ACA	GAA	GGA	GAT	ACT	CAG	TTC	523
N	W	N	I	V	S	F	P	V	A	E	E	L	S	H	H	E	N	L	V	134
AAT	TGG	AAC	ATC	GTT	TCT	TTC	CCT	GTT	GCA	GAA	GAA	CTT	TCA	CAT	CAT	GAG	AAT	CTG	GTT	583
S	F	L	E	T	V	N	Q	P	H	H	Q	N	V	S	V	P	S	N	N	154
TCA	TTT	TTA	GAA	ACT	GTG	AAC	CAG	CCA	CAC	CAC	CAC	AAT	GTG	TCT	GTG	CCC	AGC	AAT	AAT	643
V	H	A	P	Y	S	S	D	K	E	H	M	C	T	V	V	Y	F	D	D	174
GTT	CAC	GCG	CCT	TAT	TCC	AGT	GAC	AAA	GAA	CAC	CAC	ATG	TGT	ACT	GTG	GTT	TAT	TTT	GAT	703
C	M	S	I	H	Q	C	K	I	S	C	E	S	M	G	A	S	K	Y	R	194
TGC	ATG	TCC	ATA	CAT	CAG	TGT	AAA	ATA	TCC	TGT	GAG	ICC	ATG	GGA	GCA	TCC	AAA	TAT	CGC	763

FIG. 5A-2

W F H N A C C E C I G P E C I D Y G S K	214
TGG TTT CAT AAT GCC TGC TGC GAG TGC ATT GGT CCA GAA TGT ATT GAC TAT GGT AGT AAA	823
T V K C M N C M F *	224
ACT GTC AAA TGT ATG AAC TGC ATG TTT TAA	853
AGAAGACAAATGCAACCAAGCAACTTAGTAAATAATAGGTATAAAAGTTATCTGTAGTCGTGTTGTATCT	932
TGTATCAGAATCCCAGTAAGTTAAGTTGTAAAGACTTTGGGAATAAGTTTCTTTTAAATAATGACATAGCCAGTGATGT	1011
GTTTAATTATATAACTGTCTTACTGTATTTATTTGCCCCCTAGCAATAAGCCCTTTTCTTTTGAATACATGTACAACTTT	1090
GGTCATATGAGAAGCAGGTGCGCAGAGAAATTCCTTGAAAGATCTGAGGTTTTTAACATGAAGTCTGATGTGTTTCCT	1169
CTAGCATTCCAAAGGTTTTTGTCTTTTGAAAGTGTTAGCAGAACATGTTGATGTTGAATTTATGATTTCTTCATGTGCTAC	1248
TGTTAGCACACTGAGTTTTTATAGTTGCGACATCATTCCTCATTTGTCCTTTGTTTATCCATTTTATAAATAGAGTAGAT	1327
ATTTGATATACCACTCTGATAACTCATATAAAATATCATCATATAAAGCTTAAATTTTCATCCCTTTTATGTTGGTTTA	1406
AAAGGTAAATGCTTACCATAATTTTATAATTGAGAACTCTTACATAGTAGAATCCATTTCTATAATACATGTGTTGACAAA	1485
GCTTTAGAGAAAGTTTCCTATTCTCTTCCATTTTCCCTGCCCCAAAGTCTGACATAGGCAGTGATGAAGAATCTTTTACC	1564

AAGATTTTTCAGGGTGTACCTAAGAAATTGCTTTAATGCCACTGCTGGTGTAAATAATTAGCAAGCAAAAGCGTTCCTGT	1643
GACTTCAGGTACCAGCTTAAAGAGCACTAGGGATGGGGAACGAATGCCAAATCAGACTCCACCTAGAGCACCAGGAAC	1722
AGCTTGTAACCTGGTAGGGAAATGGTGTTCCTGAAAGCGGAGGCTGAGCCAGTCCGAGACTGAACCTTGTGCAGCCTTAG	1801
CCAAGACAAAGCAGTGTCTTTCAGCAGACGGCTGATGGGACAGGAATTGAAGAAGAGAATTGACTCGTATGAACAGGAC	1880
AGGGTGAAATGCTCGGGAATTATAATGGGAAACAAACTATCTATGTTCATATTTTGTAAATATTCATTTGTTAAGTTT	1959
ATATCTGGATATAATGTTCTTTTAAACAAGTATAATCATATCGTCGGAGGTTAAGATTATGAAATTTTAGAATCTCTA	2038
TTCAAGATGATGTTCACTCCAAATACACTACAGAAATTAGTCAACATTTTATATAATGTTTCAATAAATGTTTCTTTCA	2117
ATAAAAAAAAAAAAAAA	2135

FIG. 5B

FIG. 6A-1
FIG. 6A-2
FIG. 6A-3

FIG. 6A

M	P	S	L	P	A	P	P	A	P	L	L	L	L	L	L	L	L	G		20
ATG	CCG	AGC	CTC	CCG	GCC	CCG	CCG	GCC	CCG	CTG	CTG	CTC	CTC	CTG	CTG	CTG	CTC	CTC	GGC	60
S	R	P	A	R	G	A	G	P	E	P	P	V	L	P	I	R	S	E	K	40
TCC	CGG	CCG	GCC	CGC	GGC	GCC	GCC	CCA	GAG	CCC	CCC	GTG	CTG	CCC	ATC	CGT	TCT	GAG	AAG	120
E	P	L	P	V	R	G	A	A	G	C	T	F	G	G	K	V	Y	A	L	60
GAG	CCG	CTG	CCC	GTT	CGG	GGA	GCG	GCA	GCG	TGC	ACC	TTC	GGC	GGG	AAG	GTC	TAT	GCC	TTG	180

FIG. 6A-1

D	E	T	W	H	P	D	L	G	E	P	F	G	V	M	R	C	V	L	C	80
GAC	GAG	ACG	TGG	CAC	CCG	GAC	CTA	GGG	GAG	CCA	TTC	GGG	GTG	ATG	CGC	TGC	GTG	CTG	TGC	240
A	C	E	A	P	Q	W	G	R	R	T	R	G	P	G	R	V	S	C	K	100
GCC	TGC	GAG	GGG	CCT	CAG	TGG	GGT	CGC	CGT	ACC	AGG	GGC	CCT	GGC	AGG	GTC	AGC	TGC	AAG	300
N	I	K	P	E	C	P	T	P	A	C	G	Q	P	R	Q	L	P	G	H	120
AAC	ATC	AAA	CCA	GAG	TGC	CCA	ACC	CCG	GCC	TGT	GGG	CAG	CCG	CGC	CAG	CTG	CCG	GGA	CAC	360
C	C	Q	T	C	P	Q	E	R	S	S	S	E	R	Q	P	S	G	L	S	140
TGC	TGC	CAG	ACC	TGC	CCC	CAG	GAG	CGC	AGC	AGT	TCG	GAG	CGG	CAG	CCG	AGC	GGC	CTG	TCC	420
F	E	Y	P	R	D	P	E	H	R	S	Y	S	D	R	G	E	P	G	A	160
TTC	GAG	TAT	CCG	CGG	GAC	CCG	GAG	CAT	CGC	AGT	TAT	AGC	GAC	CGC	GGG	GAG	CCA	GGC	GCT	480
E	E	R	A	R	G	D	G	H	T	D	F	V	A	L	L	T	G	P	R	180
GAG	GAG	CGG	GCC	CGT	GGT	GAC	GGC	CAC	ACG	GAC	TTC	GTG	GGG	CTG	CTG	ACA	GGG	CCG	AGG	540
S	Q	A	V	A	R	A	R	V	S	L	L	R	S	S	L	R	F	S	I	200
TCG	CAG	CGG	GTG	GCA	CGC	CGA	GTC	TCG	CTG	CTG	CGC	TCT	AGC	CTC	CGC	TTC	TCT	ATC	600	
S	Y	R	R	L	D	R	P	T	R	I	R	F	S	D	S	N	G	S	V	220
TCC	TAC	AGG	CGG	CTG	GAC	CGC	CCT	ACC	AGG	ATC	CGC	TTC	TCA	GAC	TCC	AAT	GGC	AGT	GTC	660

L F E H P A A P T Q D G L V C G V W R A	240
CTG TTT GAG CAC CCT GCA GCC CCC ACC CAA GAT GGC CTG GTC TGT GGG GTG TGG CGG GCA	720
V P R L S L R L L R A E Q L H V A L V T	260
GTG CCT CGG TTG TCT CTG CCG CTC CTT AGG GCA GAA CAG CTG CAT GTG GCA CTT GTG ACA	780
L T H P S G E V W G P L I R H R A L A A	280
CTC ACT CAC CCT TCA GGG GAG GTC TGG GGG CCT CTC ATC CCG CAC CGG GCC CTG GCT GCA	840
E T F S A I L T L E G P Q Q G V G G I	300
GAG ACC TTC AGT GCC ATC CTG ACT CTA GAA GGC CCC CCA CAG CAG GGC GTA GGG GGC ATC	900
T L L T L S D T E D S L H F L L L F R G	320
ACC CTG CTC ACT CTC AGT GAC ACA GAG GAC TCC TTG CAT TTT TTG CTG CTC TTC CGA GGG	960
L L E P R S G G L T Q V P L R L Q I L H	340
CTG CTG GAA CCC AGG AGT GGG GGA CTA ACC CAG GTT CCC TTG AGG CTC CAG ATT CTA CAC	1020
Q G Q L L R E L Q A N V S A Q E P G F A	360
CAG GGG CAG CTA CTG CGA GAA CTT CAG GCC AAT GTC TCA GCC CAG GAA CCA GGC TTT GCT	1080
E V L P N L T V Q E M D W L V L G E L Q	380
GAG GTG CTG CCC AAC CTG ACA GTC CAG GAG ATG GAC TGG CTG GTG CTG GGG GAG CTG CAG	1140

FIG. 6B-1
FIG. 6B-2
FIG. 6B-3

FIG. 6B

M	A	L	E	W	A	G	R	P	G	L	R	I	S	G	H	I	A	A	R	400
ATG	GCC	CTG	GAG	TGG	GCA	GGC	AGG	CCA	GGG	CTG	CGC	ATC	AGT	GGA	CAC	ATT	GCT	GCC	AGG	1200
K	S	C	D	V	L	Q	S	V	L	C	G	A	D	A	L	I	P	V	Q	420
AAG	AGC	TGC	GAC	GTC	CTG	CAA	AGT	GTC	CTT	TGT	GGG	GCT	GAT	GCC	CTG	ATC	CCA	GTC	CAG	1260
T	G	A	A	G	S	A	S	L	T	L	L	G	N	G	S	L	I	Y	Q	440
ACG	GGT	GCT	GCC	GGC	TCA	GCC	AGC	CTC	ACG	CTG	CTA	GGA	AAT	GGC	TCC	CTG	ATC	TAT	CAG	1320

FIG. 6B-1

V Q V V G T S S E V V A M T L E T K P Q 460
 GTG CAA GTG GTA GGG ACA AGC AGT GAG GTG GTG GGC ATG ACA CTG GAG ACC AAG CCT CAG 1380

R R D Q R T V L C H M A G L Q P G G H T 480
 CGG AGG GAT CAG CGC ACT GTC CTG TGC CAC ATG GCT GGA CTC CAG CCA GGA CAC ACG 1440

A V G I C P G L G A R G A H M L L Q N E 500
 GCC GTG GGT ATC TGC CCT CGG CTG GGT GCC CGA GGG GCT CAT ATG CTG CTG CAG AAT GAG 1500

L F L N V G T K D F P D G E L R G H V A 520
 CTC TTC CTG AAC GTG GGC ACC AAG GAC TTC CCA GAC GGA GAG CTT CGG GGG CAC GTG GCT 1560

A L P Y C G H S A R H D T L S V P L A G 540
 GCC CTG CCC TAC TGT GGG CAT AGC GCC CGC CAT GAC ACG CTG TCC GTG CCC CTA GCA GGA 1620

A L V L P P V K S Q A A G H A W L S L D 560
 GCC CTG GTG CTA CCC CCT GTG AAG AGC CAA GCA GCA GGG CAC GCC TGG CTT TCC TTG GAT 1680

T H C H L H Y E V L L A G L G G S E Q G 580
 ACC CAC TGT CAC CTG CAC TAT GAA GTG CTG CTG GCT GGT GGT GGC TCA GAA CAA GGC 1740

T V T A H L L G P P G T P G P R R L L K 600
 ACT GTC ACT GCC CAC CTC CTT GGG CCT CCT GGA ACG CCA GGG CCT CGG CCG CTG CTG AAG 1800

G F Y G S E A Q G V V K D L E P E L L R 620
 GGA TTC TAT GGC TCA GAG GCC CAG GGT GTG GTG AAG GAC CTG GAG CCG GAA CTG CTG CGG 1860

H L A K G M A S L M I T T K G S P R G E 640
 CAC CTG GCA AAA GGC ATG GCC TCC CTG ATG ATC ACC AAG GGT AGC CCC AGA GGG GAG 1920

L R G Q R R T V I C D P V V C P P P S C 660
 CTC CGA GGG CAG AGA CGA ACG GTG ATC TGT GAC CCG GTG GTG TGC CCA CCG CCC AGC TGC 1980

P H P V Q A P D Q C C C P V C P E K Q D V 680
 CCA CAC CCG GTG CAG GCT CCC GAC CAG TGC TGC CCT GGT TGC CCT GAG AAA CAA GAT GTC 2040

R D L P G L P R S R D P G E G C Y F D G 700
 AGA GAC TTG CCA GGG CTG CCA AGG AGC CCG GAC CCA GGA GAG GGC TGC TAT TTT GAT GGT 2100

D R S W R A A G T R W H P V V P P F G L 720
 GAC CGG AGC TGG CGG GCA GCG GGT ACG CCG TGG CAC CCC GTT GTG CCC CCC TTT GGC TTA 2160

I K C A V C T C K G G T G E V H C E K V 740
 ATT AAG TGT GCT GTC TGC ACC TGC AAG GGG GGC ACT GGA GAG GTG CAC TGT GAG AAG GTG 2220

Q C P R L A C A Q P V R V N P T D C C K 760
 CAG TGT CCC CCG CTG GCC TGT GCC CAG CCT GTG CGT GTC AAC CCC ACC GAC TGC TGC AAA 2280

FIG. 6C-1
FIG. 6C-2

FIG. 6C

Q	C	P	V	G	S	G	A	H	P	Q	L	G	D	P	M	Q	A	D	G	780
CAG	TGT	CCA	GTG	GGG	TCG	GGG	GCC	CAC	CCC	CAG	GTG	GGG	GAC	CCC	ATG	CAG	GCT	GAT	GGG	2340
P	R	G	C	R	F	A	G	Q	W	F	P	E	S	Q	S	W	H	P	S	800
CCC	CGG	GGC	TGC	CGT	TTT	GCT	GGG	CAG	TGG	TTC	CCA	GAG	AGT	CAG	AGC	TGG	CAC	CCC	TCA	2400
V	P	P	F	G	E	M	S	C	I	T	C	R	C	G	A	G	V	P	H	820
GTG	CCC	CCT	TTT	GGA	GAG	ATG	AGC	TGT	ATC	ACC	TGC	AGA	TGT	GGG	GCA	GGG	GTG	CCT	CAC	2460

FIG. 6C-1

Applicant: Douglas A. Holtzman et al.
Title: NOVEL GENES ENCODING PROTEINS HAVING
 PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC
 AND OTHER USES

Attorney/Agent: Jean M. Silveri

Docket No.: MPI2000-540OMNI(M)

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[illegible]

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FIG. 6C-2

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APPAPLLLLLGLLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGG 60
..|: ||::|::: | ::::.....|||..|.|||. :::| |||||
QCPPIILLVWTLWIM....AVDCSRPKVFLPIQPEQEPLQSKTPAGCTFGG 47
.
KVYALDETWHPDLDGEPFGVMRCVLCACEAPQWGRRTRGPGRVSCKNIKPE 110
|.|.|:..| ||||| |||||: ||| || :||:|..|:| ||||| |.:
KFYSLEDSWHPDLGEPFGVMHCVLCYCE.PQRSRRGKPSGKVSCKNIKHD 96
.
CPTPACGQPRQLPGHCCQTCPQERSSSSERQPSGL..SFEYPRDPEHRSYS 158
|||.|.|:..| || |||.|||..... :... : :||| :... |.
CPSPSCANPILLPLHCCKTCPKAPPPPIKKSDFVFDGFEYFQEKDDDLYN 146
.
DRGEPGAEERARGDGHTDFVALLTGPR.....SQAVARARVSLLRSSLR 202
||: :... | ::::..: |||||:|. . :||:|..| ||. |
DRSYLSSDDVAVEESRSEYVALLTAPSHVWPPVTSGVAKARFNLQRSNLL 196
.
FSISYRRLDRPTRIRFSDSNGSVLFEHPA...APTQDGLVCGVWRAVPRL 249
|||.|:..: || .||| ||| :||| ||||. :...|: :||:|..: |
FSITYKWIDRLSRIRFSDLDGSVLFEHPVHRMGSPRDDTICGIWRS LNRS 246
.
SLRLLRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQ 299
.||||| ::: |.||| | ...|:..|:..:|:| |.|.|||:| | :...:
TLRLLRMGHILVSLVTTTLSEPEISGKIVKHKALFSESFSALLTPEDSDE 296
.
QGVGGITLLTSLDTEDSLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQL 349
|.||:..: |||||.:|.|||:|:| || :. :. |:|: :| | |.:
TGGGGLAMLTLSDVDDNLHFILMLRGLSGEED...QIPILVQISHQNHV 343
.
LRELQANVSAQEPGFAEVLPNLTVQEMDWLVLGELQMALEWAGRPGLRIS 399
:||| ||: ||||.: |||||:|. .|| ||. |:|:..:..: .||.. :|
IRELYANISAEQDFAEVLPDLSSREMLWLAQGQLEISVQTEGRRPQSMS 393
.
GHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGNGSLIYQVQVV 449
| |..| |||||. |||||:|: ||| |..|||. |||||:| | :||. | |:|:..
GIITVRKSCDTLQSVLSGGDALNPTKTGAVGSASITLHENGTTLEYQIQIA 443

FIG. 7A

```
GTSSEVAMTLETKPQRRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAH 499
|||.|.|.:|||||.|:..|.:|.|. .:|:.|. |. :.| |:|
GTMSTVTAVTLETKPRRKTKRNLHDMSKDYHDGR.VWGYWIDANARDLH 492
.      .      .      .      .
MLLQNELFLNVGTKDFPDGELRGHVAAALPYCGHSARHDTLSVPLAGALVL 549
|||||.|||||:|||||.:|||||:~::~| |.:| .|||.:.|.| |||||.:.:|
MLLQSELFLNVATKDFQEGELRGQITPLLYSGLWARYEKLPVPLAQFVS 542
.      .      .      .      .
PPVKSAAGHAWLSLDTHCHLHYEVLLVGLGGSEQGTVTAHLLG..... 593
||:~::~.|||||:|||||.|||||:~::~.|||||.|:~::~.|||||
PPIRTGSAGHAWVSLDEHCHLHYQIVVTGLGKAEDAALNAHLHGFAELGE 592
.      .      .      .      .
.PPGTPGPRRLKGFYGSEAQGCVKDLEPELLRHLLAKGMASLMITTKGSP 642
~::~.||.:||||| |||||: ||| |||.:.| | : ~::|||.|
VGESSPGHKRLLKGFYGSEAQGSVKDLDELLELGHLSRGTAFIQVSTKLNP 642
.      .      .      .      .
RGELRG..... 648
|||:||
RGEIRGQIHIPNSCESGGVSLTPEEPEYEYEIYEGRQRDPDDL RKDPRA 692
.      .      .      .      .
..... QRRTVICDPVVCP PPSCPHPVQA 671
|:|||||:|||||.|.:||:
CSFEGQLRAHGSRWAPDYDRKCSVCS CQKRTVICDPIVC PPLNCSQPVHL 742
.      .      .      .      .
PDQCCPVCPEKQDV RDLPGLPRSRDPGEGCYFDGDRSWRAAGTRWH PVVP 721
||||| |||.||.:~::|:~:.|.|.|.:.| |:| |:| |:| |:| |:| |:| |:|
PDQCCPVCEEKKEMREVKKPERAR.TSEGCF FDGDRSWKAAGTRWHPFVP 791
.      .      .      .      .
PFGLIKCAVCTCKGGTG EVHCEKVQC PRLACAQPV RVNPTDCCKQCPVGS 771
||||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
PFGLIKCAICTCKGSTGEVHCEKVTCPKLSCTNP I RANPSDCCKQCPVEE 841
.      .      .      .      .
GAHPQLGDPMQADGPRGCRFAGQWF PESQSWHPSVPPFGEM SCITCR CGA 821
.. |:|:|.||.||: |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
RSPMELADSMQSDGAGSCRFRHWYP NHERWHPTVPPFGEMKC VTCTCAE 891
```

FIG. 7B

GVPHCERDDCSLPLSCGSGKESRCCSRC.....TAHRRPAPETRTDPEL 865
|:::| |::|. . :...:| .|||.::|: ...|||. .:
GITQCRRQECTGTTTCGTGSKRDRCCCTKCKDANQDEDEKVKSDETRTPWSF 941

FIG. 7C

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